

Figure 1A

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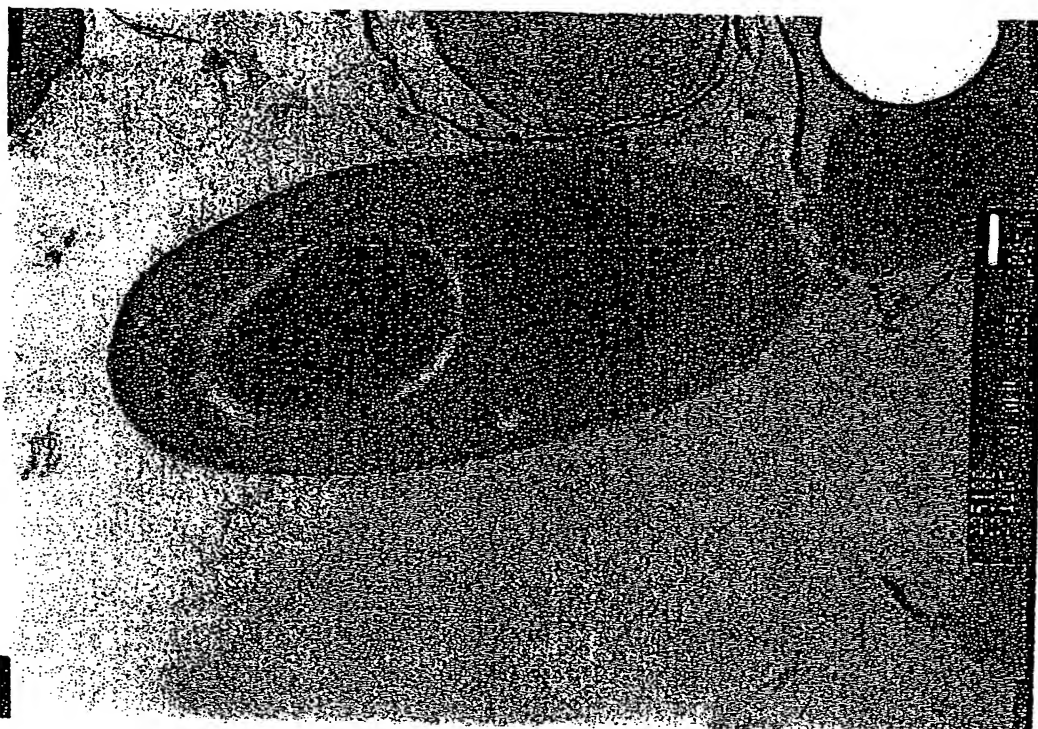


Figure 1B

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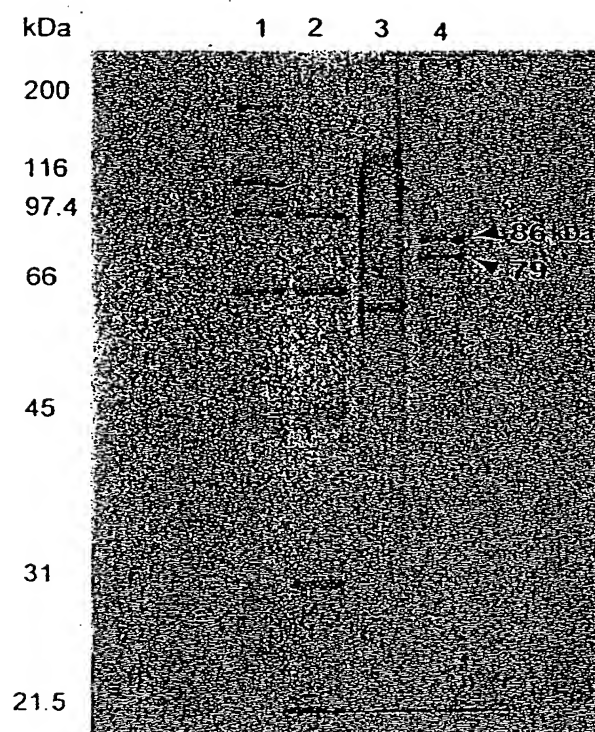


Figure 2

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Figure 3

M	D	P	F	S	N	Y	S	E	Q	K	Y	Y	P	D	D	S	N	N	N	N	N	N	N
Q	E	L	I	T	E	S	S	S	F	I	S	L	K	T	F	D	D	N	N	Q	Q	E	E
M	K	T	Y	Y	P	I	Q	Q	D	I	I	S	N	S	N	S	N	N	Q	N	N	M	M
F	P	D	N	V	N	Q	T	S	D	V	S	N	N	N	N	N	N	N	I	I	S	N	S
K	T	E	I	L	C	R	R	L	P	P	V	N	N	T	T	P	P	S	S	M	Q	P	A
M	R	N	T	S	D	I	V	I	P	P	V	N	N	S	S	S	S	S	F	P	L	I	P
D	N	L	R	H	M	N	A	G	A	A	V	N	N	T	T	T	T	T	M	A	S	L	N
I	K	F	S	N	V	A	Y	V	E	G	K	N	N	I	I	I	I	I	S	P	A	L	L
L	T	Q	A	K	F	D	M	I	F	I	Q	R	R	A	A	A	A	A	N	L	S	L	L
S	A	R	Q	S	V	Y	V	V	Q	T	R	V	I	W	E	A	W	A	N	K	A	I	L
G	W	H	N	M	I	D	V	V	S	F	W	L	L	A	A	A	A	N	A	R	S	L	L
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N	N	S	M	K	A	L	V	V	Q	Q	I	E	R	D	A	Q	A	A	R	S	N	A	L
N	N	S	M	K	A	L	V	V															

Cry31Aa2:	1	MDFPSNYSEQYPDSNNNQELITESSSFYSDTTNNENMKTYHPIEQDILKFANQEFDPNYY	60
Cry31Aa1:	1	*****K*****A*N*****T****S**H*	60
Cry31Aa2:	61	QHSDVSNSYQNMKTEIVNTDLPTYNTNNINSMRNTLCRDLPPETNMSIYDNLIRSTVTVPFS	120
Cry31Aa1:	61	*****D*****K*****	101
Cry31Aa2:	121	SNQFDPIKFLHDI EIAIETGSFSALTQSNMNQGGTDIAPMLISTFFKVAGSLLPFPLSSL	180
Cry31Aa1:	102	*****Q*****N*****S*****	161
Cry31Aa2:	181	GALAS FYVTD SQTGAMANLWRQMVDYVEKRIDSKILDYHNFIMGAELAALNASLKEYARV	240
Cry31Aa1:	162	*****	221
Cry31Aa2:	241	VKIFENDMNR ¹ IAEPPSTGVITQFRILNDNFIKYIAKLQFSTNQSDLOYPVLTLP ¹ LRAQAC	300
Cry31Aa1:	222	***** ¹ *****	281
		Block 1 (Continued)	
Cry31Aa2:	301	V ¹ MHLM ¹ LLKDATT ¹ SV ¹ MGQOIDSQOLNGYKAELIRLIKVYTNDVNTTYNOGLELEKAKPLNY	360
Cry31Aa1:	282	*****	341
		Block 2	
Cry31Aa2:	361	SDPEEYLQAGR ¹ PDISVLRSNFKEVMK ¹ W ¹ NKVAKYK ¹ RG ¹ MAMSALS ¹ LAAL ¹ FPTFGPNYPKQAL	420
Cry31Aa1:	342	*****R*****	401
		Block 2 (Continued)	
Cry31Aa2:	421	KVVQS ¹ RQIFAPVIGIPGGITSQDSGPTFGSMREFDVKTYDQIDALRQLMELYIQPLKSAYF	480
Cry31Aa1:	402	*****HSG*****R*****	461
Cry31Aa2:	481	WIYESDWKVRATYVNDYIGKRG ¹ SNTGA ¹ AH ¹ MWSSDPSAIYTSALGAAGYAPNVVGVRYS	540
Cry31Aa1:	462	Y*****L*G*****V*****	521
		Block 3	
Cry31Aa2:	541	GGSYTKGMAPANTNAYAPFEFKYPGYKLHSVSAYGLSKAPDAADSV ¹ MGFRPV ¹ LENEAN	600
Cry31Aa1:	522	*****p*****T*****	581
		Block 3 (Continued)	
Cry31Aa2:	601	QLLTD ¹ TALQI ¹ PAEIGITDVVPAFGRTEEPINGQDAIRIWESFTSGFGFTYTVDS ¹ PQKQKY	660
Cry31Aa1:	582	*****I*****	641
		Block 4 (Continued)	
Cry31Aa2:	661	KIIYRIANNLSASTVSLTYNNQTF ¹ TDILNTSLDPNGVRGNYGSYTLVEGP ¹ II ¹ EF ¹ SQGTN	720
Cry31Aa1:	642	*****	701
		Block 5	
Cry31Aa2:	721	IFKLGSQKGEFAIDS ¹ II ¹ FSPVV	742
Cry31Aa1:	702	****R*****S	723

Figure 5

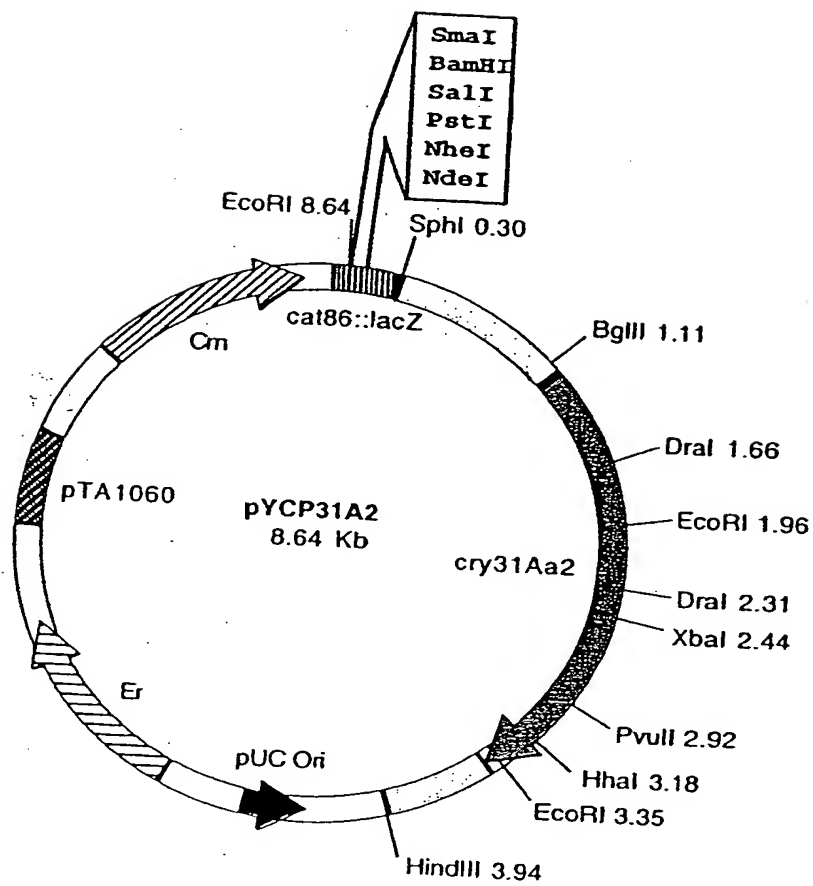


Figure 6

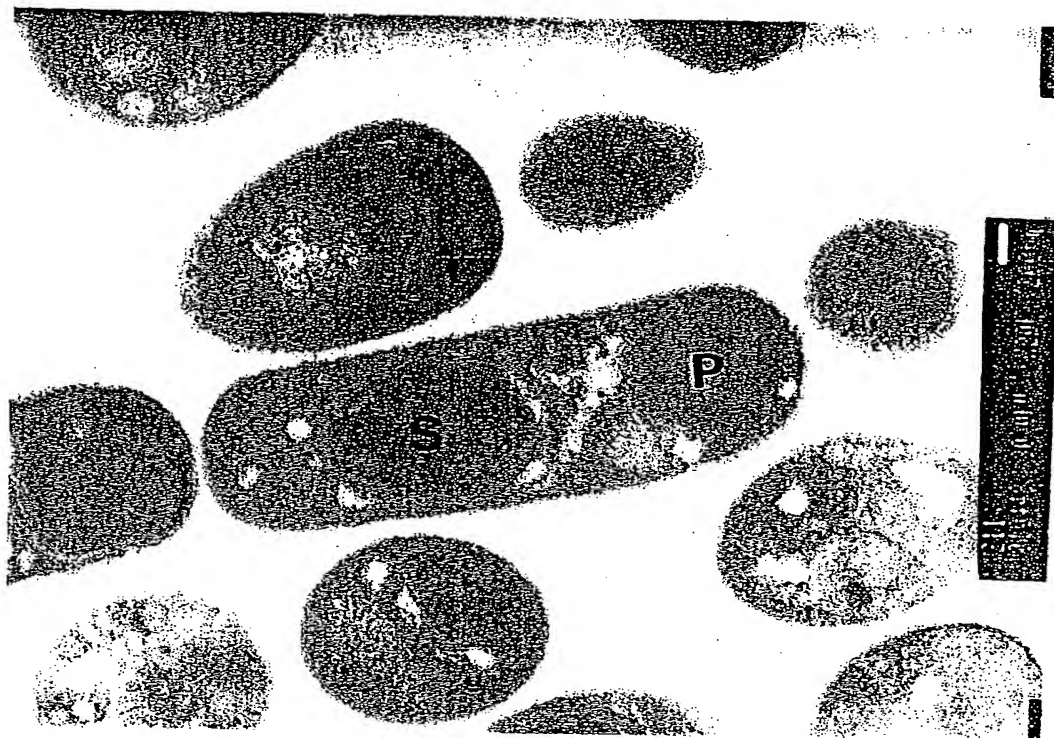


Figure 7

BEST AVAILABLE COPY

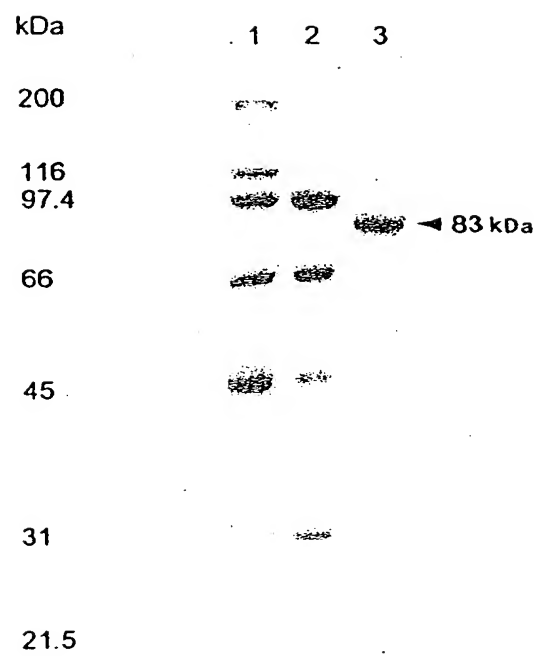


Figure 8

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-35 -10
ACTGTATACATTTTTAGTCTTATCTTTGAGTTTTTATATATTTTAAAGTTTGTGGATAAATTTTCAGGAAAAAAGATCTCAACGACTTTTGTATGTCGGT 510

GARCARAARTAYCCNGAY
TGTTTACTATGTCAAAGGTGGAGATATTGTGGACCCATTTTCTAATTATTCTGAACAAAAATACCCAGATTCAAATAATAACCAAGAACTAATTACAGAATC 612
RBS M D P F S N Y S E Q K Y P D S N N N Q E L I T E S
CTCTTCATTTTATTCGGATACTACTAATGAAAATATGAAAACCTTACCATCCAATTGAACAAGATATTCTCAAATTTGCAAATCAAGAATTTCCCGATAATTA 714
S S F Y S D T T N E N M K T Y H P I E Q D I L K F A N Q E F P D N Y
TTATCAACAATTCGATGTTTCTAATTCATATCAAAATATGAAAACAGAAATCGTAAATACAGATTTACCCCTATAATACAAATAATATAAATAGTATGCGAAA 816
Y Q H S D V S N S Y Q N M K T E I V N T D L P Y N N T N N S M R N
TACTCTAGCAGAGATTTACCTCCGAGACTAACATGACATTATGATAATTTACGATTCTACTGTTCTCTTCTTCTAATCAATTTGATCCTAT 918
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K F L H D I E I A I E T G S F S A L T Q S N M N Q G G T D I A P M L
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ATTAATGCAAGTTTAAAGAAATACGCACGAGTAGTTAAATTTTTGAAAATGATATGAACAGAATAGCTGAACCACTTCAACTGGAGTTATCACTCAATT 1326
L N A S L K E Y A R V V K I F E N D M N R I A E P P S T G V I T Q F
CAGAATCTTAATGATAATTTCAATATATATTGAAAATTACAATCTCAACAAATCAATCAGATTTACAATATCCTGTCTTAACCTTACCTACGTG 1428
R I L N D N F I K Y I A K L Q F S T N Q S D L Q Y P V L T L P L R A
ACAAGCATGTGAATGCATTTAATGTTATTAAGATGCAACGACTTCTGTGTGGGACAACAATAGACTCGCAACAATTAATGGGTATAAAGCAGAATT 1530
Q A C V M H L M L L K D A T T S V W G Q Q I D S Q Q L N G Y K A E L
AATACGTTTAATAAAAGTATATACTAATGATGTAACACAACGTAATCAAGGGCTAGAGCTAGAAAAAGCTAAACCACTAAATTAATCTGATCCTGAAGA 1632
I R L I K V Y T N D V N T T Y N Q G L E L E K A K P L N Y S D P E E
ATATTTACAAGCAGGACGTCAGATATATCTGTATTACGAGTAACCTTAAAGAGGTTATGAAGTGAATAAAGTAGCGAAATATAAAGCTGGAATGGCTAT 1734
Y L Q A G R P D I S V L R S N F K E V M K W N K V A K Y K R G M A M
GAGTGCTTTATCATTAGCTGCATTATTTCCAACCTTTCGGACCAAATTTCCAAAACAAGCATTAAAAAGTTGTGCAATCTAGACAAATTTTGCACCTGTAAT 1836
S A L A A L F P T F G P N Y P K Q A L K V V Q S R Q I F A P V I
TGAATACCAGGCGGTATACAAGTCAAGATAGTGGTCCCACTTTTGGTAGTATGAGATTGATGAAAACTTATGATCAATTTGATCGGTTACGACAAC 1938
G I P G G I T S Q D S G P T F G S M R F D V K T Y D Q I D A L R Q L
AATGGAATTATATATCTTAAATCTGCTTACTTTTGGATATATGAATCGGATTGGAAGTTCTGTCAACTTATGTCAATGATTATATTGGTAAAAG 2040
M E L Y I Q P L K S A Y F W I Y E S D W K V R A T Y V N D Y I G K R
AGGGTCAATACAGGTGCTGCTTGGCACATGTGGTCAAGTGATCCTTCAGCCATATACACTTCTGCACTAGGAGCAGCAGGATACGCTCCTAACGTTGTTGG 2142
G S N T G A A W H M W S S D P S A I Y T S A L G A A G Y A P N V V G
TGTAAGATATTCACATGGGGGTAGTTACACAAAAGGTATGGCACCCGCAAATACTAATGCGTATGCTCCATTTGAATTTAAATATCCTGGTTATAAATACTACA 2244
V R Y S H G G S Y T K G M A P A N T N A Y A P F E F K Y P G Y K L H
CAGTGTTAGTGCTTATGGATTAAGTAAAGCACCTGATGCAGCTGATTCTGTTATGTTGGATTTAGACCTGATTGTTAGAAAATGAAGCAAATCAATTATT 2346
S V S A Y G L S K A P D A A D S V M F G F R P V L L E N E A N Q L L
AACAGATACAGCATTGCAAAATCCAGCAGAAATAGGAATAACAGATGTGCTACCTGCATTGGTAGAACAGAAGAACCTATTAAATGGTCAAGATGCAATAAG 2448
T D T A L Q I P A E I G I T D V V P A F G R T E E P I N G Q D A I R
AATATGGGAAAGTTTACAAGTGGATTGGCTTTACTTATAGTGTGATTCTCCACAAAAACAAAAATATAAAATCATTATAGAATTGCAAAATAACTTAAG 2550
I W E S F T S G F G F T Y T V D S P Q K Q K Y K I I Y R I A N N L S
CGCTTCTACAGTTTCTTTAACCTATAATAATCAAAACATTTTCACTGATATTTTAAATCTTCAATAGATCCAAATGGAGTAAGAGGAAATTTATGGTTCTTA 2652
A S T V S L T Y N N Q T F F T D I L N T S L D P N G V R G N Y G S Y
TACACTGTAGAAGGCTTATTATTGAATTTTCTCAAGGAACATAATCTTTAACTAGGATCACAAAAAGGAGAATTCGCTATAGATTCCATTATTTTATAG 2754
T L V E G P I I E F S Q G T N I F K L G S Q K G E F A I D S I I F S
TCCTGTTGTTTAAATAGTGTAGTACCATTAGACCCAGACCCATGGTTTCCAGTCCAGAATATTTCCCGAGATTTCATAGTATGCTTCGATCCCGCATGTTTTAT 2856
P V V
GTACAAACACATCCTTTTTAGATAGCATTCCAATTATAGGGATGCTCTTTTTTGTATTTCTGGCCTATCCTTCTCATTTTCATAGATTTTTAATTAGTACCCT 2958

TTACAAAAAGTAACCCACCATCTTCGAACAAATCTTTGATTTCTATTTTAAAGAATAATCAATCTGTTGAACAAATTTATAAATCTTTTGAAGAGAATTTCA 3060
TTTTATTTGTTTCGCTTAAGTTGATAGGCATGTGGTTCTACCCCTAATAAGGTGTCACAGAACATAATTCTAAGACATTTCATCGTAAAAAATAGTAAATTCA 3162
TACAATACAGTTAAACTTTTCTCAGTAGCTCAGTTTTTCGATTTTCGGGTGTTTTACTCATTTCCCCCTTTGTTTTTAGGAGAGAGTGCTGGCTGGGGTT 3264
TGGGGGCTAGCCCCAAGAACTTAACGTAACGAATATGGAATAAGCTT 3313

Figure 5

GTGGACCCGTTTTCTAATTATTCTGAACAAAAATACCCAGATTCAAATAATAACCAAGAACTAATTACAAAATCC
TCTTCATTTTATTTCGGATACTACTAATGAAAATGCAAAAATTACCACCCAATTGAACAAGATATTCTCAAATTT
ACAAATCAAGAATTTTCCGATAATCATTATCAACATTCCGATGTTTCAAATGATATAAAATAGTATGCGAAATACT
CTATGCAAAGATTTACCTCCTGAGACTAACATGAGCATTATGATAATTTACGATCTACTGTTACTGTTTCCTTCA
TTTTCTAATCAATTTGATCCTATAAAATTTCTTCACGATATTGAAATTGCTATACAAACTGGATCATTTTCTGCA
TTAACGCAATCTAACATGAATCAAGGTGGTACTGATATTAATCCAATGTTAATCTCTACATTTTTTAAAGTTGCA
AGTAGTTTACTTCCATTTCTCTATCATCATTAGGTGCTTTAGCTTCCTTTTATGTTACAGATTCCAAAACAGGC
GCTATGGCAAATTTATGGAGACAAATGGTAGATTATGTTGAAAAAAGAATTGATTCTAAAATATTAGATTATCAT
AATTTTATTATGGGAGCAGAACTCGCAGCATTAAATGCAAGTTTAAAAGAATACGCACGAGTAGTTAAAATTTTT
GAAAATGATATGAACAGAATGGCTGAACCACCTTCAACTGGAGTTATCACTCAATTCAGAAATCTTAATGATAAT
TTCATTAAATACATTGCAAAATTACAATTCACAACAAATCAATCAGATTTACAATATCCTGTCCCTAACTTTACCA
TTACGTGCACAAGCATGTGTAATGCATTTAATGTTATTAAAGATGCAACGACTTCTGTGTGGGGACAACAAATA
GACTCGCAACAATTAAATGGGTATAAAGCAGAATTAATACGTTTAATAAAAAGTATATACTAATGATGTAAACACA
ACGTATAATCAAGGGCTAGAGCTAGAAAAAGCTAAACCACTAAATTATTCTGATCCTGAAGAATATTTACAAGCA
GGGCGTCCAGATATATCTGTATTACGCAGTAACTTTAAAGAGGTATGAAGTGGAATAGAGTAGCGAAATATAAA
CGTGGAATGGCTATGAGTGCTTTATCATTAGCTGCATTATTTCCAACTTTCGGACCAAATTATCCAAAACAAGCA
TTAAAAGTTGTGCAATCTAGACAAATTTTTGCACCTGTAATTGGAATACCAGGCGGTATAACAAGTCAAGATCAT
TCTGGCACTTTTGGTAGTATGAGATTTGATGTAAAAACTTATGATCAAATTGATGCGTTACGACGACTAATGGAA
TTATATATTCAACCTTTAAAATCTGCCTACTTCTATATATATGAATCGGATTGGAAAAGTTCGTGCAACTTATGTC
AATGACTATATTGGTAAAAGAGGGTCTAATACAGGTCTTGCCTGGGGAATGTGGTCAAGTGATCCTTCAGTCATA
TACACTTCTGCACTAGGAGCAGCAGGATACGCTCCTAACGTTGTTGGTGTAAGATATTCACATGGGGGTAGTTAC
ACAAAAGGTATGGCACCCCCAAATACTAATGCGTATGCTCCATTTGAATTTAAATATCCTGGTTATAAACTACAC
AGTGTTAGTGCTTATGGATTAAGTAAAGCACCTGATACAGCTGATTCTGTTATGTTTGGATTTAGACCTGTATTG
TTAGAAAATGAAGCAAATCAATTATTAACAGATACAGCATTGCAAATTCAGCAGAAAATAGGAATAACAGATGTC
GTACCTGCATTTGGTAGAACAGAAGAACCTATTAATGGTCAAGATGCAATAATAATATGGGAAAGTTTTACAAGT
GGATTTGGCTTTACTTATACTGTTGATTCTCCACAAAACAAAAATATAAAATCATTATAGAATTGCAAATAAC
TTAAGCGCTTCTACAGTTTCTTTAACCTATAATAATCAAACATTTTTTCACTGATATTTTAAATACCTCATTAGAT
CCAAATGGAGTAAGAGGAAATTATGGTTCTTATACACTTGTAGAAGGTCCTATTATTGAATTTTCTCAAGGAAC
AATATCTTTAAACTAAGATCACAAAAGGAGAATTCGCTATAGATTCCATTATTTTTAGTCCGTTCATAA

Figure 10